

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/692,077 E  
Source: JFW/6  
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IFW16

## RAW SEQUENCE LISTING

DATE: 10/19/2005

PATENT APPLICATION: US/09/692,077E

TIME: 08:48:38

Input Set : A:\10738-43s.ST25.txt

Output Set: N:\CRF4\10192005\I692077E.raw

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3 <110> APPLICANT: Liggett, Stephen
4     Small, Kersten M.
6 <120> TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
8 <130> FILE REFERENCE: 10738-43
10 <140> CURRENT APPLICATION NUMBER: 09/692,077E
11 <141> CURRENT FILING DATE: 2000-10-19
13 <160> NUMBER OF SEQ ID NOS: 26
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1353
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
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27 cgctcgctgc gcgcccctca gaacctgttc ctggtgtcgc tggccgcgcg cgacatcctg      180
29 gtggccacgc tcatcatccc tttctcgctg gccaacgagc tgctgggcta ctggtacttc      240
31 cggcgcacgt ggtgcgaggt gtacctggcg ctcgacgtgc tcttctgcac ctcgccatc      300
33 gtgcacctgt gcgccatcag cctggaccgc tactgggccg tgagccgcgc gctggagtac      360
35 aactccaagc gcaccccgcg ccgcacaaag tgcacatcc tcaactgtgt gctcatcgcc      420
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39 cgcccccagt gcaagctcaa ccaggaggcc tgggtacatcc tggcctccag catcggatct      540
41 ttctttgctc cttgcctcat catgatcctt gtctacctgc gcatctacct gatcgccaaa      600
43 cgagcaacc gcagagggtcc caggggcaag ggggggcctg ggcagggtga gtccaagcag      660
45 ccccgaccg accatggtgg ggctttggcc tcagccaaac tgccagccct ggccctctgtg      720
47 gcttctgcca gagagggtcaa cggacactcg aagtcactg gggagaagga ggagggggag      780
49 acccctgaag atactgggac ccgggccttg ccacccagtt gggctgccct tcccaactca      840
51 ggccagggcc agaaggaggg tgtttgtggg gcatctccag aggatgaagc tgaagaggag      900
53 gaagaggagg aggaggagga ggaagagtgt gaacccagg cagtgccagt gtctccggcc      960
55 tcagcttgca gcccccgct gcagcagcca cagggtccc ggggtgctggc caccctacgt     1020
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63 tgcaagggtg cccatggcct cttccagttc ttcttctgga tcgggtactg caacagctca     1260
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75 <400> SEQUENCE: 2
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80 cgctcgctgc gcgcccctca gaacctgttc ctggtgtcgc tggccgccgc cgacatcctg      180
82 gtggccacgc tcatcatccc tttctcgctg gccaacgagc tgctgggcta ctggtacttc      240
84 cggcgcacgt ggtgcgaggt gtacctggcg ctcgacgtgc tcttctgcac ctctccatc      300
86 gtgcacctgt gcgccatcag cctggaccgc tactgggccc tgagccgcgc gctggagtac      360
88 aactccaagc gcaccccgcg ccgcatcaag tgcacatcc tactgtgtg gctcatcgcc      420
90 gccgtcatct cgctgccgcc cctcatctac aaggcgacc agggcccca gccgcgcggg      480
92 cgccccagt gcaagctcaa ccaggaggcc tggtagatcc tggcctccag catcggatct      540
94 ttctttgctc cttgcctcat catgatcctt gtctacctgc gcatctacct gatcgccaaa      600
96 cgcagcaacc gcagagggtcc cagggccaag ggggggctg ggcagggtga gtccaagcag      660
98 ccccgacccg accatgggtg ggctttggcc tcagccaaac tgccagccct ggctctgtg      720
100 gcttctgcca gagagggtcaa cggacactcg aagtccactg gggagaagga ggagggggag      780
102 acccctgaag atactgggac ccgggccttg ccaccagtt gggctgccct tcccaactca      840
104 ggccaggggc agaaggaggg tgtttgtggg gcatctccag aggatgaagc tgaagaggag      900
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108 agcccccgcg tgcagcagcc acagggtccc cgggtgctgg ccaccctacg tggccagggtg      1020
110 ctccctgggca ggggcgtggg tgctataggt gggcagtggt ggcgtcgaag ggcgcagctg      1080
112 acccggggaga agcgcttcac ctctgtgctg gctgtggtca ttggcgtttt tgtgctctgc      1140
114 tggttccccct tcttcttcag ctacagcctg ggcgccatct gcccgaaagca ctgcaagggtg      1200
116 ccccatggcc tcttccagtt cttcttctgg atcggctact gcaacagctc actgaaccct      1260
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133 <211> LENGTH: 9
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135 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 4
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142 <211> LENGTH: 9
143 <212> TYPE: DNA
144 <213> ORGANISM: Homo sapiens
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147 ctctcttc      9
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151 <211> LENGTH: 9
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155 <400> SEQUENCE: 6
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159 <210> SEQ ID NO: 7
160 <211> LENGTH: 450
161 <212> TYPE: PRT
162 <213> ORGANISM: Homo sapiens

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164 &lt;400&gt; SEQUENCE: 7

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170 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
171          20          25          30
174 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
175          35          40          45
178 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
179          50          55          60
182 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
183 65          70          75          80
186 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
187          85          90          95
190 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
191          100          105          110
194 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
195          115          120          125
198 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
199          130          135          140
202 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
203 145          150          155          160
206 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
207          165          170          175
210 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
211          180          185          190
214 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
215          195          200          205
218 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
219          210          215          220
222 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
223 225          230          235          240
226 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
227          245          250          255
230 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
231          260          265          270
234 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
235          275          280          285
238 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
239          290          295          300
242 Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
243 305          310          315          320
246 Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
247          325          330          335
250 Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
251          340          345          350
254 Gly Gly Gln Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg
255          355          360          365
258 Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
259          370          375          380

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262 Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
263 385          390          395          400
266 Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
267          405          410          415
270 Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
271          420          425          430
274 Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
275          435          440          445
278 Ala Trp
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283 <211> LENGTH: 447
284 <212> TYPE: PRT
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287 <400> SEQUENCE: 8
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293 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
294          20          25          30
297 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
298          35          40          45
301 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
302          50          55          60
305 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
306 65          70          75          80
309 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
310          85          90          95
313 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
314          100          105          110
317 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
318          115          120          125
321 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
322          130          135          140
325 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
326 145          150          155          160
329 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
330          165          170          175
333 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
334          180          185          190
337 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
338          195          200          205
341 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
342          210          215          220
345 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
346 225          230          235          240
349 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
350          245          250          255
353 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
354          260          265          270

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357 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
358      275      280      285
361 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
362      290      295      300
365 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
366 305      310      315      320
369 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
370      325      330      335
373 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
374      340      345      350
377 Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg Phe Thr Phe
378      355      360      365
381 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
382      370      375      380
385 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
386 385      390      395      400
389 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
390      405      410      415
393 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
394      420      425      430
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398      435      440      445
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404 <213> ORGANISM: Homo sapiens
406 <400> SEQUENCE: 9
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409 1      5      10      15
412 <210> SEQ ID NO: 10
413 <211> LENGTH: 13
414 <212> TYPE: PRT
415 <213> ORGANISM: Homo sapiens
417 <400> SEQUENCE: 10
419 Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu Glu
420 1      5      10
423 <210> SEQ ID NO: 11
424 <211> LENGTH: 3
425 <212> TYPE: PRT
426 <213> ORGANISM: Homo sapiens
428 <400> SEQUENCE: 11
430 Glu Glu Glu
431 1
434 <210> SEQ ID NO: 12
435 <211> LENGTH: 3
436 <212> TYPE: PRT
437 <213> ORGANISM: Homo sapiens
439 <400> SEQUENCE: 12
441 Cys Glu Pro

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**VERIFICATION SUMMARY**

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